



SEQUENCE LISTING

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Stephen A. JOBLING

<120> Production of Antibodies

<130> 060113/0275850 - T7060C

<140> US 09/737,476

<141> 2000-12-18

<150> EP 99310188.0

<151> 1999-12-17

<160> 67

<170> MS Word

<210> 1

<211> 440

<212> DNA

<213> Artificial

<220>

<223> VHH with peptide linker

<220>

<221> CDS

<222> (1)..(417)

<400> 1

cag	gtg	cag	ctg	cag	gag	tca	ggg	gga	gga	ttg	gtg	cag	gct	ggg	ggc	48
Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala	Gly	Gly	
1				5						10					15	
tct	ctg	aga	ctc	tcc	tgt	gca	gcc	tcg	gga	cgc	gcc	acc	agt	ggt	cat	96
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Arg	Ala	Thr	Ser	Gly	His	
			20					25					30			
ggt	cac	tat	ggt	atg	ggc	tgg	ttc	cgc	cag	gtt	cca	ggg	aag	gag	cgt	144
Gly	His	Tyr	Gly	Met	Gly	Trp	Phe	Arg	Gln	Val	Pro	Gly	Lys	Glu	Arg	
			35				40					45				
gag	ttt	gtc	gca	gct	att	agg	tgg	agt	ggt	aaa	gag	aca	tgg	tat	aaa	192
Glu	Phe	Val	Ala	Ala	Ile	Arg	Trp	Ser	Gly	Lys	Glu	Thr	Trp	Tyr	Lys	
			50				55					60				

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
130 135

<210> 3

<211> 11

<212> PRT

<213> Artificial

<220>

<223> myc linker

<400> 3

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
1 5 10

<210> 4

<211> 471

<212> DNA

<213> Artificial

<220>

<223> VHH with linker

<220>

<221> CDS

<222> (1)..(459)

<400> 4

cag gtg cag ctg cag cag tca ggg gga ggc ttg gtg cag gct ggg ggg 48
Gln Val Gln Leu Gln Gln Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

tct ctg aga ctc tcc tgt gta gct tct gaa agc agc ttc agc aac aat 96
Ser Leu Arg Leu Ser Cys Val Ala Ser Glu Ser Ser Phe Ser Asn Asn
20 25 30

cac atg ggc tgg tac cgc cgg gct cca ggg aac cag cgc gag ctg gtc 144
His Met Gly Trp Tyr Arg Arg Ala Pro Gly Asn Gln Arg Glu Leu Val
35 40 45

gca act att agt cct ggt ggt agc aca cac tat gta gac tcc gtg aag 192
Ala Thr Ile Ser Pro Gly Gly Ser Thr His Tyr Val Asp Ser Val Lys
50 55 60

ggc cga ttc acc atc tcc cga gac aac gcc aag aac aca gtg tat cta	240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu	
65 70 75 80	
caa atg gac agc ctg aaa cca gag gac acg gcc gtc tat tac tgt gct	288
Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala	
85 90 95	
gcc aag ggg agg ggg ctg cag gct atg cag tac tgg ggc cag ggg acc	336
Ala Lys Gly Arg Gly Leu Gln Ala Met Gln Tyr Trp Gly Gln Gly Thr	
100 105 110	
ctg gtc acc gtc tcc tca gcg cac cac agc gaa gac ccc agc tcc gcg	384
Leu Val Thr Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala	
115 120 125	
gcc gcc cat cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc	432
Ala Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile	
130 135 140	
tca gaa gag gat ctg aat ggg gcc gca tagtaacaat tg	471
Ser Glu Glu Asp Leu Asn Gly Ala Ala	
145 150	

<210> 5

<211> 153

<212> PRT

<213> Artificial

<220>

<223> VHH with linker

<400> 5

Gln Val Gln Leu Gln Gln Ser Gly Gly Gly Leu Val Gln Ala Gly Gly	
1 5 10 15	
Ser Leu Arg Leu Ser Cys Val Ala Ser Glu Ser Ser Phe Ser Asn Asn	
20 25 30	
His Met Gly Trp Tyr Arg Arg Ala Pro Gly Asn Gln Arg Glu Leu Val	
35 40 45	
Ala Thr Ile Ser Pro Gly Gly Ser Thr His Tyr Val Asp Ser Val Lys	
50 55 60	
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu	
65 70 75 80	
Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala	
85 90 95	
Ala Lys Gly Arg Gly Leu Gln Ala Met Gln Tyr Trp Gly Gln Gly Thr	
100 105 110	

Leu Val Thr Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala
 115 120 125
 Ala Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile
 130 135 140
 Ser Glu Glu Asp Leu Asn Gly Ala Ala
 145 150

<210> 6

<211> 468

<212> DNA

<213> Artificial

<220>

<223> VHH with linker

<220>

<221> CDS

<222> (1)..(456)

<400> 6

cag gtg cag ctg cag gag tct ggg gga ggc ctg gtg cag gct ggg ggg	48
Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly	
1 5 10 15	
tct ctg aga ctc tcc tgt gta gcc tct gga aac acc ttc agt atc ata	96
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Asn Thr Phe Ser Ile Ile	
20 25 30	
gct atg gcc tgg tac cgc cag gct cca ggg aag cag cgc gag gtg gtc	144
Ala Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Val Val	
35 40 45	
gca agt att aat agt att ggc agc aca aat tat gca gac tcc gtg aag	192
Ala Ser Ile Asn Ser Ile Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys	
50 55 60	
ggg cga ttc acc atc tcc aga gac aac gcc aag aac aca gtg tat ctg	240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu	
65 70 75 80	
caa atg agc agc ctg aaa cct gag gac acg gcc gtc tat tac tgt gct	288
Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala	
85 90 95	
gcc ggt aat ttg ctg gtt aag agg cct tac tgg ggc cag ggg acc ctg	336
Ala Gly Asn Leu Leu Val Lys Arg Pro Tyr Trp Gly Gln Gly Thr Leu	
100 105 110	
gtc acc gtc tcc tca gaa ccc aag aca cca aaa cca caa cca gcg gcc	384
Val Thr Val Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala	
115 120 125	

gcc cat cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca 432
 Ala His His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser
 130 135 140

gaa gag gat ctg aat ggg gcc gca tagtaacaat tg 468
 Glu Glu Asp Leu Asn Gly Ala Ala
 145 150

<210> 7

<211> 152

<212> PRT

<213> Artificial

<220>

<223> VHH with linker

<400> 7

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Asn Thr Phe Ser Ile Ile
 20 25 30

Ala Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Val Val
 35 40 45

Ala Ser Ile Asn Ser Ile Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
 65 70 75 80

Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Ala Gly Asn Leu Leu Val Lys Arg Pro Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala
 115 120 125

Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser
 130 135 140

Glu Glu Asp Leu Asn Gly Ala Ala
 145 150

<210> 8

<211> 462

<212> DNA

<213> Artificial

<220>

<223> VHH with linker

<220>

<221> CDS

<222> (1)..(450)

<400> 8

acc atg gcc cag gtg aaa ctg cag cag tct ggg gga gga ttg gtg cag	48
Thr Met Ala Gln Val Lys Leu Gln Gln Ser Gly Gly Gly Leu Val Gln	
1 5 10 15	

gct ggg ggc cct ctg agg ctc tcc tgt gca gcc tct gga cgc acc ttc	96
Ala Gly Gly Pro Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe	
20 25 30	

agt aac tat gcc gtg ggc tgg ttc cgc cag gct cca ggg aag gag cgt	144
Ser Asn Tyr Ala Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg	
35 40 45	

gag ttt gtc gct gct att agc cgt gat ggt ggg cgc aca tac tat gcg	192
Glu Phe Val Ala Ala Ile Ser Arg Asp Gly Gly Arg Thr Tyr Tyr Ala	
50 55 60	

gac tcc gtg aag ggc cga ttc gcc gtc tcc aga gac tac gcc gag aac	240
Asp Ser Val Lys Gly Arg Phe Ala Val Ser Arg Asp Tyr Ala Glu Asn	
65 70 75 80	

acg gtg tat ctg caa atg aac agc ctg aaa cct gag gac acg gcc gtt	288
Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val	
85 90 95	

tat tac tgt aac aca agg gcc tac tgg ggc cag ggg acc cag gtc acc	336
Tyr Tyr Cys Asn Thr Arg Ala Tyr Trp Gly Gln Gly Thr Gln Val Thr	
100 105 110	

gtc tcc tca gcg cac cac agc gaa gac ccc agc tcc gcg gcc gcc cat	384
Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala Ala Ala His	
115 120 125	

cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca gaa gag	432
His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu	
130 135 140	

gat ctg aat ggg gcc gca tagtaacaat tg	462
Asp Leu Asn Gly Ala Ala	
145 150	

<210> 9

<211> 150

<212> PRT

<213> Artificial

<220>

<223> VHH with linker

<400> 9

Thr	Met	Ala	Gln	Val	Lys	Leu	Gln	Gln	Ser	Gly	Gly	Gly	Leu	Val	Gln	
1				5					10					15		
Ala	Gly	Gly	Pro	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Arg	Thr	Phe	
			20					25					30			
Ser	Asn	Tyr	Ala	Val	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	
	35						40					45				
Glu	Phe	Val	Ala	Ala	Ile	Ser	Arg	Asp	Gly	Gly	Arg	Thr	Tyr	Tyr	Ala	
	50					55					60					
Asp	Ser	Val	Lys	Gly	Arg	Phe	Ala	Val	Ser	Arg	Asp	Tyr	Ala	Glu	Asn	
65					70					75					80	
Thr	Val	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Lys	Pro	Glu	Asp	Thr	Ala	Val	
				85					90					95		
Tyr	Tyr	Cys	Asn	Thr	Arg	Ala	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	
			100					105					110			
Val	Ser	Ser	Ala	His	His	Ser	Glu	Asp	Pro	Ser	Ser	Ala	Ala	Ala	His	
			115				120					125				
His	His	His	His	His	Gly	Ala	Ala	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	
	130					135					140					
Asp	Leu	Asn	Gly	Ala	Ala											
145					150											

<210> 10

<211> 471

<212> DNA

<213> Artificial

<220>

<223> VHH with linker

<220>

<221> CDS

<222> (1) .. (459)

<400> 10

acc atg gcc cag gtg aaa ctg cag cag tct ggg gga gga ttg gtg cag	48
Thr Met Ala Gln Val Lys Leu Gln Gln Ser Gly Gly Gly Leu Val Gln	
1 5 10 15	
gct ggg ggc cct ctg agg ctc tcc tgt gca gcc tct gga cgc acc ttc	96
Ala Gly Gly Pro Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe	
20 25 30	
agt aac tat gcc gtg ggc tgg ttc cgc cag gct cca ggg aag gag cgt	144
Ser Asn Tyr Ala Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg	
35 40 45	
gag ttt gtc gct gct att agc cgt gat ggt ggg cgc aca tac tat gcg	192
Glu Phe Val Ala Ala Ile Ser Arg Asp Gly Gly Arg Thr Tyr Tyr Ala	
50 55 60	
gac tcc gtg aag ggc cga ttc gcc gtc tcc aga gac tac gcc gag aac	240
Asp Ser Val Lys Gly Arg Phe Ala Val Ser Arg Asp Tyr Ala Glu Asn	
65 70 75 80	
acg gtg tat ctg caa atg aac agc ctg aaa cct gag gac acg gcc gtt	288
Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val	
85 90 95	
tat tac tgt aac aca agg gcc tac tgg ggc cag ggg acc cag gtc acc	336
Tyr Tyr Cys Asn Thr Arg Ala Tyr Trp Gly Gln Gly Thr Gln Val Thr	
100 105 110	
gtc tcc tca gcg cac cac agc gaa gac ccc agc tcc gcg gcc gcc cat	384
Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala Ala Ala His	
115 120 125	
cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca gaa gag	432
His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu	
130 135 140	
gat ctg aat agt gag aaa gat gag cta tgataacaat tg	471
Asp Leu Asn Ser Glu Lys Asp Glu Leu	
145 150	

<210> 11

<211> 153

<212> PRT

<213> Artificial

<220>

<223> VHH with linker

<400> 11

Thr Met Ala Gln Val Lys Leu Gln Gln Ser Gly Gly Gly Leu Val Gln
1 5 10 15
Ala Gly Gly Pro Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe
20 25 30

Ser Asn Tyr Ala Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg
 35 40 45
 Glu Phe Val Ala Ala Ile Ser Arg Asp Gly Gly Arg Thr Tyr Tyr Ala
 50 55 60
 Asp Ser Val Lys Gly Arg Phe Ala Val Ser Arg Asp Tyr Ala Glu Asn
 65 70 75 80
 Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val
 85 90 95
 Tyr Tyr Cys Asn Thr Arg Ala Tyr Trp Gly Gln Gly Thr Gln Val Thr
 100 105 110
 Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala Ala Ala His
 115 120 125
 His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu
 130 135 140
 Asp Leu Asn Ser Glu Lys Asp Glu Leu
 145 150

<210> 12

<211> 38

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 12

agctgcgac gcaagcttgg taccggaat tctctaga

38

<210> 13

<211> 42

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 13

aatttctaga gaattcccg taccaagctt gcttgcgac gc

42

<210> 14

<211> 31

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 14

tgcacccatg gcccgctagc caattggagc t

31

<210> 15

<211> 23

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 15

ccaattggct agcgggccat ggg

23

<210> 16

<211> 22

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 16

ccacccacga gggaacatcg tg

22

<210> 17

<211> 39

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 17

gaattcccat ggtttacact cgaggtcctc tccaaatga

39

<210> 18

<211> 189

<212> DNA

<213> Artificial

<220>

<223> PCR product

<400> 18

ccacccacga gggaacatcg tggaaaaaga agacgttcca accacgtctt caaagcaagt 60

ggattgatgt gatattctcca ctgacgtaag ggatgacgca caatcccact atccttcgca 120

agacccttcc tttatataag gaagttcatt tcatttggag aggacctcga gtgtaaacca 180

tgggaattc 189

<210> 19

<211> 21

<212> DNA

<213> Artificial

<220>

<223> sequencing primer

<400> 19

ccggcaacag gattcaatct t

21

<210> 20

<211> 40

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 20

agctccatgg gatttgttct cttttcaciaa ttgccttcat

40

<210> 21

<211> 35

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 21

ttcttcttgt ctctacactt ctcttattcc tagta

35

<210> 22

<211> 35

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 22

atatcccaact cttgccgtgc ccaggtgcag ctgca

35

<210> 23

<211> 48

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 23

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48

<210> 24

<211> 54

<212> DNA

<213> Artificial

<220>
 <223> synthetic insert
 <400> 24
 gtgtagagac aagaagaaat gaaggcaatt gtgaaaagag aacaaatccc atgg 54

 <210> 25
 <211> 24
 <212> DNA
 <213> Artificial
 <220>
 <223> synthetic insert
 <400> 25
 ggaaacagct atgaccatga ttac 24

 <210> 26
 <211> 20
 <212> DNA
 <213> Artificial
 <220>
 <223> synthetic insert
 <400> 26
 tttcccagtc acgacgttgt 20

 <210> 27
 <211> 107
 <212> DNA
 <213> Artificial
 <220>
 <223> synthetic fragment encoding PRIa leader
 <220>
 <221> CDS
 <222> (3) .. (104)

<400> 27

cc atg gga ttt gtt ctc ttt tca caa ttg cct tca ttt ctt ctt gtc	47
Met Gly Phe Val Leu Phe Ser Gln Leu Pro Ser Phe Leu Leu Val	
1 5 10 15	

tct aca ctt ctc tta ttc cta gta ata tcc cac tct tgc cgt gcc cag	95
Ser Thr Leu Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg Ala Gln	
20 25 30	

gtg cag ctg cag	107
Val Gln Leu	

<210> 28

<211> 34

<212> PRT

<213> Artificial

<220>

<223> synthetic fragment encoding PRIa leader

<400> 28

Met Gly Phe Val Leu Phe Ser Gln Leu Pro Ser Phe Leu Leu Val Ser	
1 5 10 15	

Thr Leu Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg Ala Gln Val	
20 25 30	

Gln Leu

<210> 29

<211> 21

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 29

gacatcccat ggcaagcatc a	21
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<210> 30

<211> 21

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 30

aagcttggtta acagccctta a

21

<210> 31

<211> 21

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 31

agggctggtta acaaacttga t

21

<210> 32

<211> 44

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 32

agactgctgc agctgcacct gcttttcaca aacaatggta gctg

44

<210> 33

<211> 19

<212> DNA

<213> Artificial

<220>

<223> sequencing primer

<400> 33

aattaaccct cactaaagg

19

<210> 34

<211> 254

<212> DNA

<213> Artificial

<220>

<223> GBSS leader

<220>

<221> CDS

<222> (3)..(254)

<400> 34

cc atg gca agc atc aca gct tca cac cac ttt gtg tca aga agc caa	47
Met Ala Ser Ile Thr Ala Ser His His Phe Val Ser Arg Ser Gln	
1 5 10 15	

act tca cta gac acc aaa tca acc ttg tca cag ata gga ctc agg aac	95
Thr Ser Leu Asp Thr Lys Ser Thr Leu Ser Gln Ile Gly Leu Arg Asn	
20 25 30	

cat act ctg act cac aat ggt tta agg gct gtt aac aaa ctt gat ggg	143
His Thr Leu Thr His Asn Gly Leu Arg Ala Val Asn Lys Leu Asp Gly	
35 40 45	

ctc caa tca aga act aat act aag gta aca ccc aag atg gca tcc aga	191
Leu Gln Ser Arg Thr Asn Thr Lys Val Thr Pro Lys Met Ala Ser Arg	
50 55 60	

act gag acc aag aga cct gga tgc tca gct acc att gtt tgt gga aaa	239
Thr Glu Thr Lys Arg Pro Gly Cys Ser Ala Thr Ile Val Cys Gly Lys	
65 70 75	

cag gtg cag ctg cag	254
Gln Val Gln Leu Gln	
80	

<210> 35

<211> 84

<212> PRT

<220>

<223> GBSS leader

<213> Artificial

<400> 35

Met	Ala	Ser	Ile	Thr	Ala	Ser	His	His	Phe	Val	Ser	Arg	Ser	Gln	Thr
1				5					10					15	
Ser	Leu	Asp	Thr	Lys	Ser	Thr	Leu	Ser	Gln	Ile	Gly	Leu	Arg	Asn	His
			20					25					30		
Thr	Leu	Thr	His	Asn	Gly	Leu	Arg	Ala	Val	Asn	Lys	Leu	Asp	Gly	Leu
		35					40					45			
Gln	Ser	Arg	Thr	Asn	Thr	Lys	Val	Thr	Pro	Lys	Met	Ala	Ser	Arg	Thr
	50					55					60				
Glu	Thr	Lys	Arg	Pro	Gly	Cys	Ser	Ala	Thr	Ile	Val	Cys	Gly	Lys	Gln
65					70					75					80

Val Gln Leu Gln

<210> 36

<211> 18

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 36

catgcaggtg cagctgca

18

<210> 37

<211> 10

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 37

gctgcacctg

10

<210> 38

<211> 24

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 38

cgcaagaccc ttcctctata taag

24

<210> 39

<211> 60

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 39

gagctcgaat tcttattata gctcatcttt ctctgaattc agatcctctt ctgagatgag

60

<210> 40

<211> 26

<212> PRT

<213> Artificial

<220>

<223> linker

<400> 40

Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr
20 25

<210> 41

<211> 20

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 41

atcctcaact tccaatcaga

20

<210> 42

<211> 19

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 42

ttcttgagag atagcttga

19

<210> 43

<211> 30

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 43

gatcccatgg cccgctagcc aattggagct

30

<210> 44

<211> 22

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 44

ccaattggct agcgggccat gg

22

<210> 45

<211> 29

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 45

gatccacctc gagtgtaaac catggcccg

29

<210> 46

<211> 29

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 46

ctagcggggc atggtttaca ctcgaggtg

29

<210> 47

<211> 20

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 47

attgcctacg gcagccgctg

20

<210> 48

<211> 51

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 48

tccaaccaat tggtactatg cggccccatt cagatcctct tctgagatga g

51

<210> 49

<211> 25

<212> DNA

<213> Artificial

<220>

<223> sequencing primer

<400> 49

gtctgtctaa agtaaagtag atgcg

25

<210> 50

<211> 60

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 50

tccaaccaat tggtatcata gtcctcttt ctcactattc agatcctctt ctgagatgag

60

<210> 51

<211> 29

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 51

agtcccccat ggtacgtcct gtagaaacc

29

<210> 52

<211> 25

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 52

cgtttttcgctc ggtaatcacc attcc

25

<210> 53

<211> 24

<212> DNA

<213> Artificial

<220>

<223> sequencing primer

<400> 53

cgcaagacccc ttcctttata taag

24

<210> 54

<211> 1154

<212> DNA

<213> Artificial

<220>

<223> HCV33-hinge-CH2-CH3

<220>

<221> CDS

<222> (3)..(1136)

<400> 54

cc atg gag gtg cag ctg cag gag tca ggg gga gga ttg gtg cag gct
Met Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala
1 5 10 15

47

ggg ggc tct ctg aga ctc tcc tgt gca gcc tcg gga cgc gcc acc agt
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser
20 25 30

95

ggc cat ggt cac tat ggt atg ggc tgg ttc cgc cag gtt cca ggg aag
Gly His Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys
35 40 45

143

gag cgt gag ttt gtc gca gct att agg tgg agt ggt aaa gag aca tgg	191
Glu Arg Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp	
50 55 60	
tat aaa gac tcc gtg aag ggc cga ttc acc atc tcc aga gat aac gcc	239
Tyr Lys Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala	
65 70 75	
aag act acg gtt tat ctg caa atg aac agc ctg aaa cct gaa gat acg	287
Lys Thr Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr	
80 85 90 95	
gcc gtt tat tat tgt gcc gct cga ccg gtc cgc gtg gat gat att tcc	335
Ala Val Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser	
100 105 110	
ctg ccg gtt ggg ttt gac tac tgg ggc cag ggg acc cag gtc acc gtc	383
Leu Pro Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val	
115 120 125	
tcc tca gaa ccc aag aca cca aaa cca caa cca caa cca cca cca	431
Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Gln Pro Gln Pro Gln	
130 135 140	
cca caa ccc aat cct aca aca gaa tcc aag tgt ccc aaa tgt cca gcc	479
Pro Gln Pro Asn Pro Thr Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala	
145 150 155	
cct gag ctc ctg gga ggg ccc tca gtc ttc atc ttc ccc ccg aaa ccc	527
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro	
160 165 170 175	
aag gac gtc ctc tcc att tct ggg agg ccc gag gtc acg tgc gtt gtg	575
Lys Asp Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val	
180 185 190	
gta gac gtg ggc cag gaa gac ccc gag gtc agt ttc aac tgg tac att	623
Val Asp Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile	
195 200 205	
gat ggc gca gag gtg cga acg gcc aac acg agg cca aaa gag gaa cag	671
Asp Gly Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln	
210 215 220	
ttc aac agc acg tac cgc gtg gtc agc gtc ctg ccc atc cag cac cag	719
Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln	
225 230 235	
gac tgg ctg acg ggg aaa gag ttc aaa tgc aag gtc aac aac aaa gct	767
Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala	
240 245 250 255	
ctc ccg gcc ccc atc gag aag acc atc tcc aag gcc aaa ggg cag acc	815
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr	
260 265 270	
cgg gag ccg cag gtg tac gcc ctg gcc cca cac cgg gaa gag ctg gcc	863
Arg Glu Pro Gln Val Tyr Ala Leu Ala Pro His Arg Glu Glu Leu Ala	
275 280 285	

aag gac acc gtg agc gta acc tgc ctg gtc aaa ggc ttc tac cca cct 911
 Lys Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro
 290 295 300

gat atc aac gtt gag tgg cag agg aac ggt cag ccg gag tca gag ggc 959
 Asp Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly
 305 310 315

acc tac gcc acc acg cca ccc cag ctg gac aac gac ggg acc tac ttc 1007
 Thr Tyr Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe
 320 325 330 335

ctc tac agc aag ctc tcg gtg gga aag aac acg tgg cag cgg gga gaa 1055
 Leu Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu
 340 345 350

acc ttc acc tgt gtg gtg atg cac gag gcc ctg cac aac cac tac acc 1103
 Thr Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr
 355 360 365

cag aaa tcc atc acc cag tct tcg ggt aaa taa taagaattcg agctcgaa 1154
 Gln Lys Ser Ile Thr Gln Ser Ser Gly Lys
 370 375

<210> 55

<211> 377

<212> PRT

<213> Artificial

<400> 55

Met Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly
 1 5 10 15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser Gly
 20 25 30

His Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys Glu
 35 40 45

Arg Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp Tyr
 50 55 60

Lys Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
 65 70 75 80

Thr Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala
 85 90 95

Val Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu
 100 105 110

Pro Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser
 115 120 125

Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Gln Pro Gln Pro Gln Pro
 130 135 140
 Gln Pro Asn Pro Thr Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala Pro
 145 150 155 160
 Glu Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys
 165 170 175
 Asp Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val Val
 180 185 190
 Asp Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile Asp
 195 200 205
 Gly Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln Phe
 210 215 220
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp
 225 230 235 240
 Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu
 245 250 255
 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr Arg
 260 265 270
 Glu Pro Gln Val Tyr Ala Leu Ala Pro His Arg Glu Glu Leu Ala Lys
 275 280 285
 Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro Asp
 290 295 300
 Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr
 305 310 315 320
 Tyr Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu
 325 330 335
 Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu Thr
 340 345 350
 Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 355 360 365
 Lys Ser Ile Thr Gln Ser Ser Gly Lys
 370 375

<210> 56

<211> 1172

<212> DNA

<213> Artificial

<220>

<223> hinge-HCV33-CH2-CH3-SEKDEL

<220>

<221> CDS

<222> (3) .. (1154)

<400> 56

cc atg gag gtg cag ctg cag gag tca ggg gga gga ttg gtg cag gct	47
Met Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala	
1 5 10 15	
ggg ggc tct ctg aga ctc tcc tgt gca gcc tcg gga cgc gcc acc agt	95
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser	
20 25 30	
ggt cat ggt cac tat ggt atg ggc tgg ttc cgc cag gtt cca ggg aag	143
Gly His Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys	
35 40 45	
gag cgt gag ttt gtc gca gct att agg tgg agt ggt aaa gag aca tgg	191
Glu Arg Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp	
50 55 60	
tat aaa gac tcc gtg aag ggc cga ttc acc atc tcc aga gat aac gcc	239
Tyr Lys Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala	
65 70 75	
aag act acg gtt tat ctg caa atg aac agc ctg aaa cct gaa gat acg	287
Lys Thr Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr	
80 85 90 95	
gcc gtt tat tat tgt gcc gct cga ccg gtc cgc gtg gat gat att tcc	335
Ala Val Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser	
100 105 110	
ctg ccg gtt ggg ttt gac tac tgg ggc cag ggg acc cag gtc acc gtc	383
Leu Pro Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val	
115 120 125	
tcc tca gaa ccc aag aca cca aaa cca caa cca caa cca cca cca	431
Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Gln Pro Gln Pro Gln	
130 135 140	
cca caa ccc aat cct aca aca gaa tcc aag tgt ccc aaa tgt cca gcc	479
Pro Gln Pro Asn Pro Thr Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala	
145 150 155	
cct gag ctc ctg gga ggg ccc tca gtc ttc atc ttc ccc ccg aaa ccc	527
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro	
160 165 170 175	
aag gac gtc ctc tcc att tct ggg agg ccc gag gtc acg tgc gtt gtg	575
Lys Asp Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val	
180 185 190	
gta gac gtg ggc cag gaa gac ccc gag gtc agt ttc aac tgg tac att	623
Val Asp Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile	
195 200 205	

gat ggc gca gag gtg cga acg gcc aac acg agg cca aaa gag gaa cag Asp Gly Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln 210 215 220	671
ttc aac agc acg tac cgc gtg gtc agc gtc ctg ccc atc cag cac cag Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln 225 230 235	719
gac tgg ctg acg ggg aaa gag ttc aaa tgc aag gtc aac aac aaa gct Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala 240 245 250 255	767
ctc ccg gcc ccc atc gag aag acc atc tcc aag gcc aaa ggg cag acc Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr 260 265 270	815
cgg gag ccg cag gtg tac gcc ctg gcc cca cac cgg gaa gag ctg gcc Arg Glu Pro Gln Val Tyr Ala Leu Ala Pro His Arg Glu Glu Leu Ala 275 280 285	863
aag gac acc gtg agc gta acc tgc ctg gtc aaa ggc ttc tac cca cct Lys Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro 290 295 300	911
gat atc aac gtt gag tgg cag agg aac ggt cag ccg gag tca gag ggc Asp Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly 305 310 315	959
acc tac gcc acc acg cca ccc cag ctg gac aac gac ggg acc tac ttc Thr Tyr Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe 320 325 330 335	1007
ctc tac agc aag ctc tcg gtg gga aag aac acg tgg cag cgg gga gaa Leu Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu 340 345 350	1055
acc ttc acc tgt gtg gtg atg cac gag gcc ctg cac aac cac tac acc Thr Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr 355 360 365	1103
cag aaa tcc atc acc cag tct tcg ggt aaa tct gag aaa gat gag cta Gln Lys Ser Ile Thr Gln Ser Ser Gly Lys Ser Glu Lys Asp Glu Leu 370 375 380	1151
taa taagaattcg agctcgaa	1172

<210> 57

<211> 383

<212> PRT

<213> Artificial

<220>

<223> hinge-HCV33-CH2-CH3-SEKDEL

<400> 57

Met Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly
 1 5 10 15
 Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser Gly
 20 25 30
 His Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys Glu
 35 40 45
 Arg Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp Tyr
 50 55 60
 Lys Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
 65 70 75 80
 Thr Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala
 85 90 95
 Val Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu
 100 105 110
 Pro Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser
 115 120 125
 Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Gln Pro Gln Pro Gln Pro
 130 135 140
 Gln Pro Asn Pro Thr Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala Pro
 145 150 155 160
 Glu Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys
 165 170 175
 Asp Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val Val
 180 185 190
 Asp Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile Asp
 195 200 205
 Gly Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln Phe
 210 215 220
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp
 225 230 235 240
 Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu
 245 250 255
 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr Arg
 260 265 270
 Glu Pro Gln Val Tyr Ala Leu Ala Pro His Arg Glu Glu Leu Ala Lys
 275 280 285
 Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro Asp
 290 295 300
 Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr
 305 310 315 320

caaatgcaag gtcaacaaca aagctc

26

<210> 61

<211> 42

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 61

ttcgagctcg aattcttatt atttaccoga agactgggtg at

42

<210> 62

<211> 27

<212> DNA

<213> Artificial

<220>

<223> sequencing primer

<400> 62

ctgaggagac ggtgacctgg gtcccct

27

<210> 63

<211> 46

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 63

agcccctgag ctctgggag ggcctcagt ctteatcttc cccccg

46

<210> 64

<211> 61

<212> DNA

<213> Artificial
 <220>
 <223> PCR primer
 <400> 64
 ttcgagctcg aattcttatt atttaccoga agactgggtg atggatttct gggtagtg 60
 g 61
 <210> 65
 <211> 79
 <212> DNA
 <213> Artificial
 <220>
 <223> PCR primer
 <400> 65
 ttcgagctcg aattcttatt atagctcatc tttctcagat ttaccgaag actgggtgat 60
 ggatttctgg gtgtagtg 79
 <210> 66
 <211> 461
 <212> DNA
 <213> Artificial
 <220>
 <223> VHH with linker
 <220>
 <221> CDS
 <222> (3)..(449)
 <400> 66
 cc atg gcc cag gtg cag ctg cag gag tct ggg gga ggc ttg gtg cag 47
 Met Ala Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln
 1 5 10 15
 gct ggg ggg tct ctg agg ctc tcc tgt gca gcc tct gga agc att ttc 95
 Ala Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe
 20 25 30

aga cgt ccg cat atg ggt tgg ttc cgc cag gct cca ggg cag gag cgc	143
Arg Arg Pro His Met Gly Trp Phe Arg Gln Ala Pro Gly Gln Glu Arg	
35 40 45	
gag ttg gtc gca ctg att tct gcg ggt ggt cgt aca tgg tat gca gac	191
Glu Leu Val Ala Leu Ile Ser Ala Gly Gly Arg Thr Trp Tyr Ala Asp	
50 55 60	
tcc gtg aag ggc cga ttc acc atc tcc aga gac aac gcc aag aac acg	239
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr	
65 70 75	
ctg tat ctg caa atg aac agc ctg aaa cct gag gac acg gcc gtt tat	287
Leu Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr	
80 85 90 95	
tac tgt act gcc ggg ggt tcg tac tgg ggc cag ggg acc cag gtc acc	335
Tyr Cys Thr Ala Gly Gly Ser Tyr Trp Gly Gln Gly Thr Gln Val Thr	
100 105 110	
gtc gcc tca gaa ccc aag aca cca aaa cca caa cca gcg gcc gcc cat	383
Val Ala Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala Ala His	
115 120 125	
cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca gaa gag	431
His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu	
130 135 140	
gat ctg aat ggg gcc gca tagtaacaat tg	461
Asp Leu Asn Gly Ala Ala	
145	

<210> 67

<211> 149

<212> PRT

<213> Artificial

<220>

<223> VHH with linker

<400> 67

Met Ala Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala	
1 5 10 15	
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Arg	
20 25 30	
Arg Pro His Met Gly Trp Phe Arg Gln Ala Pro Gly Gln Glu Arg Glu	
35 40 45	
Leu Val Ala Leu Ile Ser Ala Gly Gly Arg Thr Trp Tyr Ala Asp Ser	
50 55 60	
Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu	
65 70 75 80	

Tyr	Leu	Gln	Met	Asn	Ser	Leu	Lys	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr
				85					90					95	
Cys	Thr	Ala	Gly	Gly	Ser	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val
			100					105					110		
Ala	Ser	Glu	Pro	Lys	Thr	Pro	Lys	Pro	Gln	Pro	Ala	Ala	Ala	His	His
			115				120					125			
His	His	His	His	Gly	Ala	Ala	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp
			130			135					140				
Leu	Asn	Gly	Ala	Ala											
145															